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RAW SEQUENCE LISTING DATE: 02/06/2002
PATENT APPLICATION: US/09/843,676 TIME: 15:48:38

Input Set : N:\Crf3\RULE60\09843676.raw
Output Set: N:\CRF3\02062002\I843676.raw

SEQUENCE LISTING

ENTERED

(1) GENERAL INFORMATION:
(i) APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
(ii) TITLE OF INVENTION: Novel Telomerase
(iii) NUMBER OF SEQUENCES: 225
(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Townsend and Townsend and Crew LLP
(B) STREET: Two Embarcadero Center, 8th Floor
(C) CITY: San Francisco
(D) STATE: California
(E) COUNTRY: United States of America
(F) ZIP: 94111
(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
(vi) CURRENT APPLICATION DATA:
C--> **(A) APPLICATION NUMBER: US/09/843,676**
C--> **(B) FILING DATE: 26-Apr-2001**
(C) CLASSIFICATION: 536
(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US/08/854,050
(B) FILING DATE: 09-MAY-1997
(A) APPLICATION NUMBER: US 08/846,017
(B) FILING DATE: 25-APR-1997
(A) APPLICATION NUMBER: US 08/844,419
(B) FILING DATE: 18-APR-1997
(A) APPLICATION NUMBER: US 08/724,643
(B) FILING DATE: 01-OCT-1996
(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Apple, Randolph T.
(B) REGISTRATION NUMBER: 36,429
(C) REFERENCE/DOCKET NUMBER: 015389-002930US
(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (415) 576-0200
(B) TELEFAX: (415) 576-0300

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Input Set : N:\Crf3\RULE60\09843676.raw
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(2) INFORMATION FOR SEQ ID NO: 1:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3279 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "DNA"
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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TTAATAAGCT CAGATTTTAA ATATTAATTA CAAAACCTAA ATGGAGGTTG ATGTTGATAA 120
TCAAGCTGAT AATCATGGCA TTCACTCAGC TCTTAAGACT TGTGAAGAAA TTAAAGAAGC 180
TAAAACGTTG TACTCTTGGA TCCAGAAAGT TATTAGATGA AGAAATCAAT CTCAAAGTCA 240
TTATAAAGAT TTAGAAGATA TTAAAATATT TGCGCAGACA AATATTGTTG CTACTCCACG 300
AGACTATAAT GAAGAAGATT TTAAAGTTAT TGCAAGAAAA GAAGTATTTT CAACTGGACT 360
AATGATCGAA CTTATTGACA AATGCTTAGT TGAACTTCTT TCATCAAGCG ATGTTTCAGA 420
TAGACAAAAA CTTCAATGAT TTGGATTTCA ACTTAAGGGA AATCAATTAG CAAAGACCCA 480
TTTATTAACA GCTCTTTCAA CTCAAAAGCA GTATTTCTTT CAAGACGAAT GGAACCAAGT 540
TAGAGCAATG ATTGGAAATG AGCTCTTCCG ACATCTCTAC ACTAAATATT TAATATTCCA 600
GCGAACTTCT GAAGGAACTC TTGTTCAATT TTGCGGGAAT AACGTTTTTG ATCATTTGAA 660
AGTCAACGAT AAGTTTGACA AAAAGCAAAA AGGTGGAGCA GCAGACATGA ATGAACCTCG 720
ATGTTGATCA ACCTGCAAAT ACAATGTCAA GAATGAGAAA GATCACTTTC TCAACAACAT 780
CAACGTGCCG AATTGGAATA ATATGAAATC AAGAACCAGA ATATTTTATT GCACTCATTT 840
TAATAGAAAT AACCAATTCT TCAAAAAGCA TGAGTTTGTG AGTAACAAAA ACAATATTTC 900
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GAAGCTAAAA GATAAGGTTA TCGAAAAAAT TGCCTACATG CTTGAGAAAG TCAAAGATTT 1020
TAACTTCAAC TACTATTTAA CAAAATCTTG TCCTCTTCCA GAAAATTGGC GGGAACGGAA 1080
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CAATATACTC CCCAAAGACT TTTTGACTGG AAGAAACCGT AAGAATTTTC AAAAGAAAGT 1260
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TTCAGATTTC TGGATTATGA CTGCACAAAT TCTAAAGAGA AAGAATAACA TAGTTATCGA 2040
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TAACTTACTT CAACCAGTCA TTAATATTTG CCAATATAAT TACATTAACT TTAATGGGAA 2280
GTTTTATAAA CAAACAAAAG GAATTCCTCA AGGTCTTTGA GTTTCATCAA TTTTGTCATC 2340
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PATENT APPLICATION: US/09/843,676 TIME: 15:48:38

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158 CCCTGAAAAT CCAAATGTTA ATCTTCTAAT GAGACTTACA GATGACTATC TTTTGATTAC    2460
160 AACTCAAGAG AATAATGCAG TATTGTTTAT TGAGAAACTT ATAAACGTAA GTCGTGAAAA    2520
162 TGGATTTAAA TTCAATATGA AGAAACTACA GACTAGTTTT CCATTAAGTC CAAGCAAATT    2580
164 TGCAAAATAC GGAATGGATA GTGTTGAGGA GCAAAATATT GTTCAAGATT ACTGCGATTG    2640
166 GATTGGCATC TCAATTGATA TGAAAACTCT TGCTTTAATG CCAAATATTA ACTTGAGAAT    2700
168 AGAAGGAATT CTGTGTACAC TCAATCTAAA CATGCAAACA AAGAAAGCAT CAATGTGGCT    2760
170 CAAGAAGAAA CTAAAGTCGT TTTTAATGAA TAACATTACC CATTATTTTA GAAAGACGAT    2820
172 TACAACCGAA GACTTTGCGA ATAAAACTCT CAACAAGTTA TTTATATCAG GCGGTTACAA    2880
174 ATACATGCAA TGAGCCAAAG AATACAAGGA CCACTTTAAG AAGAACTTAG CTATGAGCAG    2940
176 TATGATCGAC TTAGAGGTAT CTAAAATTAT ATACTCTGTA ACCAGAGCAT TCTTTAAATA    3000
178 CCTTGTGTGC AATATTAAGG ATACAATTTT TGGAGAGGAG CATTATCCAG ACTTTTTCCT    3060
180 TAGCACACTG AAGCACTTTA TTGAAATATT CAGCACAAAA AAGTACATTT TCAACAGAGT    3120
182 TTGCATGATC CTCAAGGCAA AAGAAGCAAA GCTAAAAAGT GACCAATGTC AATCTCTAAT    3180
184 TCAATATGAT GCATAGTCGA CTATTCTAAC TTATTTTGGA AAGTTAATTT TCAATTTTTG    3240
186 TCTTATATAC TGGGGTTTTG GGGTTTTGGG GTTTTGGGG                           3279
188 (2) INFORMATION FOR SEQ ID NO: 2:
190      (i) SEQUENCE CHARACTERISTICS:
191           (A) LENGTH: 1031 amino acids
192           (B) TYPE: amino acid
193           (C) STRANDEDNESS: Not Relevant
W--> 194      (D) TOPOLOGY: Not Relevant
196     (ii) MOLECULE TYPE: protein
198     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
200      Met Glu Val Asp Val Asp Asn Gln Ala Asp Asn His Gly Ile His Ser
201      1               5                  10                  15
203      Ala Leu Lys Thr Cys Glu Glu Ile Lys Glu Ala Lys Thr Leu Tyr Ser
204                  20                  25                  30
206      Trp Ile Gln Lys Val Ile Arg Cys Arg Asn Gln Ser Gln Ser His Tyr
207              35                  40                  45
209      Lys Asp Leu Glu Asp Ile Lys Ile Phe Ala Gln Thr Asn Ile Val Ala
210          50                  55                  60
212      Thr Pro Arg Asp Tyr Asn Glu Glu Asp Phe Lys Val Ile Ala Arg Lys
213      65                  70                  75                  80
215      Glu Val Phe Ser Thr Gly Leu Met Ile Glu Leu Ile Asp Lys Cys Leu
216                      85                  90                  95
218      Val Glu Leu Leu Ser Ser Ser Asp Val Ser Asp Arg Gln Lys Leu Gln
219                  100                 105                 110
221      Cys Phe Gly Phe Gln Leu Lys Gly Asn Gln Leu Ala Lys Thr His Leu
222              115                 120                 125
224      Leu Thr Ala Leu Ser Thr Gln Lys Gln Tyr Phe Phe Gln Asp Glu Trp
225          130                 135                 140
227      Asn Gln Val Arg Ala Met Ile Gly Asn Glu Leu Phe Arg His Leu Tyr
228      145                 150                 155                 160
230      Thr Lys Tyr Leu Ile Phe Gln Arg Thr Ser Glu Gly Thr Leu Val Gln
231                      165                 170                 175
233      Phe Cys Gly Asn Asn Val Phe Asp His Leu Lys Val Asn Asp Lys Phe
234                  180                 185                 190
236      Asp Lys Lys Gln Lys Gly Gly Ala Ala Asp Met Asn Glu Pro Arg Cys
237              195                 200                 205
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```
239  Cys Ser Thr Cys Lys Tyr Asn Val Lys Asn Glu Lys Asp His Phe Leu
240      210                 215                 220
242  Asn Asn Ile Asn Val Pro Asn Trp Asn Asn Met Lys Ser Arg Thr Arg
243  225                 230                 235                 240
245  Ile Phe Tyr Cys Thr His Phe Asn Arg Asn Asn Gln Phe Phe Lys Lys
246                  245                 250                 255
248  His Glu Phe Val Ser Asn Lys Asn Asn Ile Ser Ala Met Asp Arg Ala
249              260                 265                 270
251  Gln Thr Ile Phe Thr Asn Ile Phe Arg Phe Asn Arg Ile Arg Lys Lys
252          275                 280                 285
254  Leu Lys Asp Lys Val Ile Glu Lys Ile Ala Tyr Met Leu Glu Lys Val
255      290                 295                 300
257  Lys Asp Phe Asn Phe Asn Tyr Tyr Leu Thr Lys Ser Cys Pro Leu Pro
258  305                 310                 315                 320
260  Glu Asn Trp Arg Glu Arg Lys Gln Lys Ile Glu Asn Leu Ile Asn Lys
261                  325                 330                 335
263  Thr Arg Glu Glu Lys Ser Lys Tyr Tyr Glu Glu Leu Phe Ser Tyr Thr
264              340                 345                 350
266  Thr Asp Asn Lys Cys Val Thr Gln Phe Ile Asn Glu Phe Phe Tyr Asn
267          355                 360                 365
269  Ile Leu Pro Lys Asp Phe Leu Thr Gly Arg Asn Arg Lys Asn Phe Gln
270      370                 375                 380
272  Lys Lys Val Lys Lys Tyr Val Glu Leu Asn Lys His Glu Leu Ile His
273  385                 390                 395                 400
275  Lys Asn Leu Leu Leu Glu Lys Ile Asn Thr Arg Glu Ile Ser Trp Met
276                  405                 410                 415
278  Gln Val Glu Thr Ser Ala Lys His Phe Tyr Tyr Phe Asp His Glu Asn
279              420                 425                 430
281  Ile Tyr Val Leu Trp Lys Leu Leu Arg Trp Ile Phe Glu Asp Leu Val
282          435                 440                 445
284  Val Ser Leu Ile Arg Cys Phe Phe Tyr Val Thr Glu Gln Gln Lys Ser
285      450                 455                 460
287  Tyr Ser Lys Thr Tyr Tyr Tyr Arg Lys Asn Ile Trp Asp Val Ile Met
288  465                 470                 475                 480
290  Lys Met Ser Ile Ala Asp Leu Lys Lys Glu Thr Leu Ala Glu Val Gln
291                  485                 490                 495
293  Glu Lys Glu Val Glu Glu Trp Lys Lys Ser Leu Gly Phe Ala Pro Gly
294              500                 505                 510
296  Lys Leu Arg Leu Ile Pro Lys Lys Thr Thr Phe Arg Pro Ile Met Thr
297          515                 520                 525
299  Phe Asn Lys Lys Ile Val Asn Ser Asp Arg Lys Thr Thr Lys Leu Thr
300      530                 535                 540
302  Thr Asn Thr Lys Leu Leu Asn Ser His Leu Met Leu Lys Thr Leu Lys
303  545                 550                 555                 560
305  Asn Arg Met Phe Lys Asp Pro Phe Gly Phe Ala Val Phe Asn Tyr Asp
306                  565                 570                 575
308  Asp Val Met Lys Lys Tyr Glu Glu Phe Val Cys Lys Trp Lys Gln Val
309              580                 585                 590
311  Gly Gln Pro Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr
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Input Set : N:\Crf3\RULE60\09843676.raw
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312                595                 600                 605
314      Asp Ser Val Asn Arg Glu Lys Leu Ser Thr Phe Leu Lys Thr Thr Lys
315          610                 615                 620
317      Leu Leu Ser Ser Asp Phe Trp Ile Met Thr Ala Gln Ile Leu Lys Arg
318      625                 630                 635                 640
320      Lys Asn Asn Ile Val Ile Asp Ser Lys Asn Phe Arg Lys Lys Glu Met
321                      645                 650                 655
323      Lys Asp Tyr Phe Arg Gln Lys Phe Gln Lys Ile Ala Leu Glu Gly Gly
324                  660                 665                 670
326      Gln Tyr Pro Thr Leu Phe Ser Val Leu Glu Asn Glu Gln Asn Asp Leu
327              675                 680                 685
329      Asn Ala Lys Lys Thr Leu Ile Val Glu Ala Lys Gln Arg Asn Tyr Phe
330          690                 695                 700
332      Lys Lys Asp Asn Leu Leu Gln Pro Val Ile Asn Ile Cys Gln Tyr Asn
333      705                 710                 715                 720
335      Tyr Ile Asn Phe Asn Gly Lys Phe Tyr Lys Gln Thr Lys Gly Ile Pro
336                      725                 730                 735
338      Gln Gly Leu Cys Val Ser Ser Ile Leu Ser Ser Phe Tyr Tyr Ala Thr
339                  740                 745                 750
341      Leu Glu Glu Ser Ser Leu Gly Phe Leu Arg Asp Glu Ser Met Asn Pro
342              755                 760                 765
344      Glu Asn Pro Asn Val Asn Leu Leu Met Arg Leu Thr Asp Asp Tyr Leu
345          770                 775                 780
347      Leu Ile Thr Thr Gln Glu Asn Asn Ala Val Leu Phe Ile Glu Lys Leu
348      785                 790                 795                 800
350      Ile Asn Val Ser Arg Glu Asn Gly Phe Lys Phe Asn Met Lys Lys Leu
351                      805                 810                 815
353      Gln Thr Ser Phe Pro Leu Ser Pro Ser Lys Phe Ala Lys Tyr Gly Met
354                  820                 825                 830
356      Asp Ser Val Glu Glu Gln Asn Ile Val Gln Asp Tyr Cys Asp Trp Ile
357              835                 840                 845
359      Gly Ile Ser Ile Asp Met Lys Thr Leu Ala Leu Met Pro Asn Ile Asn
360          850                 855                 860
362      Leu Arg Ile Glu Gly Ile Leu Cys Thr Leu Asn Leu Asn Met Gln Thr
363      865                 870                 875                 880
365      Lys Lys Ala Ser Met Trp Leu Lys Lys Lys Leu Lys Ser Phe Leu Met
366                      885                 890                 895
368      Asn Asn Ile Thr His Tyr Phe Arg Lys Thr Ile Thr Thr Glu Asp Phe
369                  900                 905                 910
371      Ala Asn Lys Thr Leu Asn Lys Leu Phe Ile Ser Gly Gly Tyr Lys Tyr
372              915                 920                 925
374      Met Gln Cys Ala Lys Glu Tyr Lys Asp His Phe Lys Lys Asn Leu Ala
375          930                 935                 940
377      Met Ser Ser Met Ile Asp Leu Glu Val Ser Lys Ile Ile Tyr Ser Val
378      945                 950                 955                 960
380      Thr Arg Ala Phe Phe Lys Tyr Leu Val Cys Asn Ile Lys Asp Thr Ile
381                      965                 970                 975
383      Phe Gly Glu Glu His Tyr Pro Asp Phe Phe Leu Ser Thr Leu Lys His
384                  980                 985                 990
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Output Set: N:\CRF3\02062002\I843676.raw

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L:33 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
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Output Set: N:\CRF3\02062002\I843676.raw

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L:7827 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217
L:7830 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217
L:7833 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217
L:7908 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217